



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/501,053

DATE: 07/16/2004

TIME: 16:48:48

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\07162004\J501053.raw

3 <110> APPLICANT: YU, Long
 5 <120> TITLE OF INVENTION: HUMAN HEPATOMA-DERIVED GROWTH FACTOR 5, ITS ENCODING
 SEQUENCE, METHOD FOR

6 PRODUCING IT AND THE USES THEREOF

8 <130> FILE REFERENCE: 017216

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/501,053

C--> 10 <141> CURRENT FILING DATE: 2004-07-09

10 <150> PRIOR APPLICATION NUMBER: CN02110535.9

11 <151> PRIOR FILING DATE: 2002-01-11

13 <160> NUMBER OF SEQ ID NOS: 8

15 <170> SOFTWARE: PatentIn version 3.1

17 <210> SEQ ID NO: 1

18 <211> LENGTH: 990

19 <212> TYPE: DNA

20 <213> ORGANISM: Homo sapiens

22 <220> FEATURE:

23 <221> NAME/KEY: CDS

24 <222> LOCATION: (5)..(910)

25 <223> OTHER INFORMATION:

W--> 28 <400> 1

29 cgct atg tct tgc ttc agc cgc cca aaa tac aag acc ggg gac ctg gtg 49
 30 Met Ser Cys Phe Ser Arg Pro Lys Tyr Lys Thr Gly Asp Leu Val
 31 1 5 10 15
 33 ttt gcc aaa tta aag ggc tat gcc cat tgg cca gcg agg att gaa cat 97
 34 Phe Ala Lys Leu Lys Gly Tyr Ala His Trp Pro Ala Arg Ile Glu His
 35 20 25 30
 37 gtc act gaa ccc aac cgc tac cag gtg ttc ttc ttc ggg acc cat gag 145
 38 Val Thr Glu Pro Asn Arg Tyr Gln Val Phe Phe Phe Gly Thr His Glu
 39 35 40 45
 41 acc gcc ctg ctg ggc ccc aag cac ctt ttt cct tat gag gag tcc aag 193
 42 Thr Ala Leu Leu Gly Pro Lys His Leu Phe Pro Tyr Glu Glu Ser Lys
 43 50 55 60
 45 gag agg ttc ggc aag cct aac aag agg cgc ggc ttc agt gag ggg ctg 241
 46 Glu Arg Phe Gly Lys Pro Asn Lys Arg Arg Gly Phe Ser Glu Gly Leu
 47 65 70 75
 49 tgg gag atc gag cac gac cct atg gct gag gcc tcc cct tgc ctg tgc 289
 50 Trp Glu Ile Glu His Asp Pro Met Ala Glu Ala Ser Pro Cys Leu Cys
 51 80 85 90 95
 53 cca gat gag gag cag ctt tgt gcc gag gag cca ggg cca gga gag gag 337
 54 Pro Asp Glu Glu Gln Leu Cys Ala Glu Glu Pro Gly Pro Gly Glu Glu
 55 100 105 110
 57 cca gag ccg ggg cag gag ctg gag ccg gaa tcc agg cct gag ctg gaa 385
 58 Pro Glu Pro Gly Gln Glu Leu Glu Pro Glu Ser Arg Pro Glu Leu Glu
 59 115 120 125



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61 tcc atg cct gag ctg gag gca gaa ccg agg cct gag aaa gag tgt gag      433
62 Ser Met Pro Glu Leu Glu Ala Glu Pro Arg Pro Glu Lys Glu Cys Glu
63      130      135      140
65 cag gag ccg gag cag gag ccg gag cag gag ctg gag cag gag ccg gag      481
66 Gln Glu Pro Glu Gln Glu Pro Glu Gln Glu Leu Glu Gln Glu Pro Glu
67      145      150      155
69 ctg gag ccg gag ccg gag ccg gag ccg gag ccg gag ccg gag ccc gag      529
70 Leu Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu
71 160      165      170      175
73 ccc gag ccg gag ccg gag ccc cag cct gcc tat gac cta ctg gat gcc      577
74 Pro Glu Pro Glu Pro Glu Pro Gln Pro Ala Tyr Asp Leu Leu Asp Ala
75      180      185      190
77 aag gag gag cct ggc ctc att gag gcc gag cca gga gat cag caa gcc      625
78 Lys Glu Glu Pro Gly Leu Ile Glu Ala Glu Pro Gly Asp Gln Gln Ala
79      195      200      205
81 gag caa gtg cga gag cag cac gct gaa gct gag gtc atg gct gta gtg      673
82 Glu Gln Val Arg Glu Gln His Ala Glu Ala Glu Val Met Ala Val Val
83      210      215      220
85 gag gag ccg gag agt ctg aag agg agc gcg gag gat gaa cag cct cac      721
86 Glu Glu Pro Glu Ser Leu Lys Arg Ser Ala Glu Asp Glu Gln Pro His
87      225      230      235
89 agt cct ccc aaa cgg ccc agg gag gcg gcg cct ggc gcg ctg gag atg      769
90 Ser Pro Pro Lys Arg Pro Arg Glu Ala Ala Pro Gly Ala Leu Glu Met
91 240      245      250      255
93 gag ccg gct gga gag cgc gag gca gag gcc tgc ccc ttc gtg gag gag      817
94 Glu Pro Ala Gly Glu Arg Glu Ala Glu Ala Cys Pro Phe Val Glu Glu
95      260      265      270
97 cct gac caa gcc cag gaa cag cag act ccg ttg gaa gaa gag gcc aca      865
98 Pro Asp Gln Ala Gln Glu Gln Gln Thr Pro Leu Glu Glu Glu Ala Thr
99      275      280      285
101 gag gag gca gtc cag ggc ctg atg gtt gga gaa atc gaa ggc ctg      910
102 Glu Glu Ala Val Gln Gly Leu Met Val Gly Glu Ile Glu Gly Leu
103      290      295      300
105 tagtcacggt gtctgtaaaa gagccctctc taccggttcc tgggtgccacc tggctgtggc      970
107 ttgggaaacc cgctagggcc      990
110 <210> SEQ ID NO: 2
111 <211> LENGTH: 302
112 <212> TYPE: PRT
113 <213> ORGANISM: Homo sapiens
115 <400> SEQUENCE: 2
117 Met Ser Cys Phe Ser Arg Pro Lys Tyr Lys Thr Gly Asp Leu Val Phe
118 1      5      10      15
121 Ala Lys Leu Lys Gly Tyr Ala His Trp Pro Ala Arg Ile Glu His Val
122      20      25      30
125 Thr Glu Pro Asn Arg Tyr Gln Val Phe Phe Phe Gly Thr His Glu Thr
126      35      40      45
129 Ala Leu Leu Gly Pro Lys His Leu Phe Pro Tyr Glu Glu Ser Lys Glu
130      50      55      60
133 Arg Phe Gly Lys Pro Asn Lys Arg Arg Gly Phe Ser Glu Gly Leu Trp

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134 65          70          75          80
137 Glu Ile Glu His Asp Pro Met Ala Glu Ala Ser Pro Cys Leu Cys Pro
138          85          90          95
141 Asp Glu Glu Gln Leu Cys Ala Glu Glu Pro Gly Pro Gly Glu Glu Pro
142          100          105          110
145 Glu Pro Gly Gln Glu Leu Glu Pro Glu Ser Arg Pro Glu Leu Glu Ser
146          115          120          125
149 Met Pro Glu Leu Glu Ala Glu Pro Arg Pro Glu Lys Glu Cys Glu Gln
150          130          135          140
153 Glu Pro Glu Gln Glu Pro Glu Gln Glu Leu Glu Gln Glu Pro Glu Leu
154 145          150          155          160
157 Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro
158          165          170          175
161 Glu Pro Glu Pro Glu Pro Gln Pro Ala Tyr Asp Leu Leu Asp Ala Lys
162          180          185          190
165 Glu Glu Pro Gly Leu Ile Glu Ala Glu Pro Gly Asp Gln Gln Ala Glu
166          195          200          205
169 Gln Val Arg Glu Gln His Ala Glu Ala Glu Val Met Ala Val Val Glu
170          210          215          220
173 Glu Pro Glu Ser Leu Lys Arg Ser Ala Glu Asp Glu Gln Pro His Ser
174 225          230          235          240
177 Pro Pro Lys Arg Pro Arg Glu Ala Ala Pro Gly Ala Leu Glu Met Glu
178          245          250          255
181 Pro Ala Gly Glu Arg Glu Ala Glu Ala Cys Pro Phe Val Glu Glu Pro
182          260          265          270
185 Asp Gln Ala Gln Glu Gln Gln Thr Pro Leu Glu Glu Glu Ala Thr Glu
186          275          280          285
189 Glu Ala Val Gln Gly Leu Met Val Gly Glu Ile Glu Gly Leu
190          290          295          300

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193 <210> SEQ ID NO: 3

194 <211> LENGTH: 21

195 <212> TYPE: DNA

196 <213> ORGANISM: Artificial sequence

198 <220> FEATURE:

199 <221> NAME/KEY: misc_feature

200 <222> LOCATION: (1)..(21)

201 <223> OTHER INFORMATION: primer

204 <400> SEQUENCE: 3

205 cgctatgtct tgcttcagcc g

21

208 <210> SEQ ID NO: 4

209 <211> LENGTH: 21

210 <212> TYPE: DNA

211 <213> ORGANISM: Artificial sequence

213 <220> FEATURE:

214 <221> NAME/KEY: misc_feature

215 <222> LOCATION: (1)..(21)

216 <223> OTHER INFORMATION: primer

219 <400> SEQUENCE: 4

220 ggccctagcg ggtttcccaa g

21

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Input Set : A:\PTO.FG.txt

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223 <210> SEQ ID NO: 5
224 <211> LENGTH: 27
225 <212> TYPE: DNA
226 <213> ORGANISM: Artificial sequence
228 <220> FEATURE:
229 <221> NAME/KEY: misc_feature
230 <222> LOCATION: (1)..(27)
231 <223> OTHER INFORMATION: primer
234 <400> SEQUENCE: 5
235 gcaggatcca tgtcttgctt cagccgc 27
238 <210> SEQ ID NO: 6
239 <211> LENGTH: 27
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial sequence
243 <220> FEATURE:
244 <221> NAME/KEY: misc_feature
245 <222> LOCATION: (1)..(27)
246 <223> OTHER INFORMATION: primer
249 <400> SEQUENCE: 6
250 ccgaagcttc aggccttcga tttctcc 27
253 <210> SEQ ID NO: 7
254 <211> LENGTH: 27
255 <212> TYPE: DNA
256 <213> ORGANISM: Artificial sequence
258 <220> FEATURE:
259 <221> NAME/KEY: misc_feature
260 <222> LOCATION: (1)..(27)
261 <223> OTHER INFORMATION: primer
264 <400> SEQUENCE: 7
265 gcaaagctta tgtcttgctt cagccgc 27
268 <210> SEQ ID NO: 8
269 <211> LENGTH: 27
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial sequence
273 <220> FEATURE:
274 <221> NAME/KEY: misc_feature
275 <222> LOCATION: (1)..(27)
276 <223> OTHER INFORMATION: primer
279 <400> SEQUENCE: 8
280 ccgggatccc aggccttcga tttctcc 27

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/501,053

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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY

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Input Set : A:\PTO.FG.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:28 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:25